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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/892,864A

DATE: 01/26/2002

TIME: 12:44:35

Input Set : A:\209524US0CONT.txt

Output Set: N:\CRF3\01262002\I892864A.raw

ENTERED

5 <110> APPLICANT: YOKOYAMA, Keiichi  
7 ONO, Kunio  
9 EJIMA, Daisuke  
13 <120> TITLE OF INVENTION: PROCESS FOR PRODUCING TRANSGLUTAMINASE  
17 <130> FILE REFERENCE: 209524US0CONT  
21 <140> CURRENT APPLICATION NUMBER: US/09/892,864A  
23 <141> CURRENT FILING DATE: 2001-06-28  
27 <150> PRIOR APPLICATION NUMBER: PCT/JP99/07250  
29 <151> PRIOR FILING DATE: 1999-12-24  
33 <150> PRIOR APPLICATION NUMBER: JP 10-373131  
35 <151> PRIOR FILING DATE: 1998-12-28  
39 <160> NUMBER OF SEQ ID NOS: 58  
43 <170> SOFTWARE: PatentIn version 3.1  
47 <210> SEQ ID NO: 1  
49 <211> LENGTH: 1519  
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53 <213> ORGANISM: Artificial Sequence  
57 <220> FEATURE:  
59 <223> OTHER INFORMATION: Synthetic DNA  
61 <220> FEATURE:  
63 <221> NAME/KEY: CDS  
65 <222> LOCATION: (87)..(1082)  
67 <223> OTHER INFORMATION:  
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74 ggtatcgtatt agtaaggagg tttaaa atg gat tct gac gat cgt gtt act cca 113  
75 Met Asp Ser Asp Asp Arg Val Thr Pro  
76 1 5  
78 cca gct gaa cca ctg gat cgt atg cca gat cca tat cgt cca tct tat 161  
79 Pro Ala Glu Pro Leu Asp Arg Met Pro Asp Pro Tyr Arg Pro Ser Tyr  
80 10 15 20 25  
82 ggt cgt gct gaa act gtt gtt aat aat tat att cgt aaa tgg caa caa 209  
83 Gly Arg Ala Glu Thr Val Val Asn Asn Tyr Ile Arg Lys Trp Gln Gln  
84 30 35 40  
86 gtt tat tct cat cgt gat ggt cgt aaa caa caa atg act gaa gaa caa 257  
87 Val Tyr Ser His Arg Asp Gly Arg Lys Gln Gln Met Thr Glu Glu Gln  
88 45 50 55  
90 cgt gaa tgg ctg tct tat ggt tgc gtt ggt gtt act tgg gtt aac tct 305  
91 Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly Val Thr Trp Val Asn Ser  
92 60 65 70  
94 ggt cag tat ccg act aac cgt ctg gca ttc gct tcc ttc gat gaa gat 353  
95 Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe Ala Ser Phe Asp Glu Asp  
96 75 80 85

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98 cgt ttc aag aac gaa ctg aag aac ggt cgt ccg cgt tct ggt gaa act      401
99 Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg Pro Arg Ser Gly Glu Thr
100 90                               95                               100                               105
102 cgt gct gaa ttc gaa ggt cgt gtt gct aag gaa tcc ttc gat gaa gag      449
103 Arg Ala Glu Phe Glu Gly Arg Val Ala Lys Glu Ser Phe Asp Glu Glu
104                               110                               115                               120
106 aaa ggc ttc cag cgt gct cgt gaa gtt gct tct gtt atg aac cgt gct      497
107 Lys Gly Phe Gln Arg Ala Arg Glu Val Ala Ser Val Met Asn Arg Ala
108                               125                               130                               135
110 cta gag aac gct cat gat gaa tct gct tac ctg gat aac ctg aag aag      545
111 Leu Glu Asn Ala His Asp Glu Ser Ala Tyr Leu Asp Asn Leu Lys Lys
112                               140                               145                               150
114 gaa ctg gct aac ggt aac gat gct ctg cgt aac gaa gat gct cgt tct      593
115 Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg Asn Glu Asp Ala Arg Ser
116                               155                               160                               165
118 ccg ttc tac tct gct ctg cgt aac act ccg tcc ttc aaa gaa cgt aac      641
119 Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro Ser Phe Lys Glu Arg Asn
120 170                               175                               180                               185
122 ggt ggt aac cat gat ccg tct cgt atg aaa gct gtt atc tac tct aaa      689
123 Gly Gly Asn His Asp Pro Ser Arg Met Lys Ala Val Ile Tyr Ser Lys
124                               190                               195                               200
126 cat ttc tgg tct ggt cag gat aga tct tct tct gct gat aaa cgt aaa      737
127 His Phe Trp Ser Gly Gln Asp Arg Ser Ser Ser Ala Asp Lys Arg Lys
128                               205                               210                               215
130 tac ggt gat ccg gat gca ttc cgt ccg gct ccg ggt act ggt ctg gta      785
131 Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala Pro Gly Thr Gly Leu Val
132                               220                               225                               230
134 gac atg tct cgt gat cgt aac atc ccg cgt tct ccg act tct ccg ggt      833
135 Asp Met Ser Arg Asp Arg Asn Ile Pro Arg Ser Pro Thr Ser Pro Gly
136                               235                               240                               245
138 gaa ggc ttc gtt aac ttc gat tac ggt tgg ttc ggt gct cag act gaa      881
139 Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp Phe Gly Ala Gln Thr Glu
140 250                               255                               260                               265
142 gct gat gct gat aag act gta tgg acc cat ggt aac cat tac cat gct      929
143 Ala Asp Ala Asp Lys Thr Val Trp Thr His Gly Asn His Tyr His Ala
144                               270                               275                               280
146 ccg aac ggt tct ctg ggt gct atg cat gta tac gaa tct aaa ttc cgt      977
147 Pro Asn Gly Ser Leu Gly Ala Met His Val Tyr Glu Ser Lys Phe Arg
148                               285                               290                               295
150 aac tgg tct gaa ggt tac tct gac ttc gat cgt ggt gct tac gtt atc      1025
151 Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp Arg Gly Ala Tyr Val Ile
152                               300                               305                               310
154 acc ttc att ccg aaa tct tgg aac act gct ccg gac aaa gtt aaa cag      1073
155 Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala Pro Asp Lys Val Lys Gln
156                               315                               320                               325
158 ggt tgg ccg taatgaaagc ttggatctct aattactgga cttcacacag      1122
159 Gly Trp Pro
160 330
162 actaaaatag acatatctta tattatgtga ttttgtgaca tttcctagat gtgaggtgga      1182

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164 ggtgatgtat aaggtagatg atgatacctct acgcccggacg catcgtggcc ggcatacccg 1242
166 gcgccacagg tgcggttgct ggcgcctata tcgccgacat caccgatggg gaagatcggg 1302
168 ctgccactt cgggctcatg agcgcttggt tcggcgtggg tatggtggca ggccccgtgg 1362
170 ccgggggact gttgggcgcc atctccttgc atgcaccatt ccttgccggcg gcggtgctca 1422
172 acggcctcaa cctactactg ggctgcttcc taatgcagga gtcgcataag ggagagcgtc 1482
174 gagagcccg ctaatgagcg ggcttttttt tcagctg 1519
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179 <211> LENGTH: 332
181 <212> TYPE: PRT
183 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
189 <223> OTHER INFORMATION: Synthetic Peptide
191 <400> SEQUENCE: 2
193 Met Asp Ser Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg
194 1 5 10 15
197 Met Pro Asp Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val
198 20 25 30
201 Asn Asn Tyr Ile Arg Lys Trp Gln Val Tyr Ser His Arg Asp Gly
202 35 40 45
205 Arg Lys Gln Gln Met Thr Glu Gln Arg Glu Trp Leu Ser Tyr Gly
206 50 55 60
209 Cys Val Gly Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg
210 65 70 75 80
213 Leu Ala Phe Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys
214 85 90 95
217 Asn Gly Arg Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg
218 100 105 110
221 Val Ala Lys Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg
222 115 120 125
225 Glu Val Ala Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu
226 130 135 140
229 Ser Ala Tyr Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp
230 145 150 155 160
233 Ala Leu Arg Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg
234 165 170 175
237 Asn Thr Pro Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser
238 180 185 190
241 Arg Met Lys Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp
242 195 200 205
245 Arg Ser Ser Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe
246 210 215 220
249 Arg Pro Ala Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn
250 225 230 235 240
253 Ile Pro Arg Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp
254 245 250 255
257 Tyr Gly Trp Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val
258 260 265 270
261 Trp Thr His Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala
262 275 280 285

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265 Met His Val Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser
266      290      295      300
269 Asp Phe Asp Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp
270 305      310      315      320
273 Asn Thr Ala Pro Asp Lys Val Lys Gln Gly Trp Pro
274      325      330
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279 <211> LENGTH: 39
281 <212> TYPE: DNA
283 <213> ORGANISM: Artificial Sequence
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289 <223> OTHER INFORMATION: Synthetic DNA
291 <400> SEQUENCE: 3
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297 <211> LENGTH: 41
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301 <213> ORGANISM: Artificial Sequence
305 <220> FEATURE:
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315 <211> LENGTH: 41
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319 <213> ORGANISM: Artificial Sequence
323 <220> FEATURE:
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327 <400> SEQUENCE: 5
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333 <211> LENGTH: 41
335 <212> TYPE: DNA
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341 <220> FEATURE:
343 <223> OTHER INFORMATION: Synthetic DNA
345 <400> SEQUENCE: 6
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355 <213> ORGANISM: Artificial Sequence
359 <220> FEATURE:
361 <223> OTHER INFORMATION: Synthetic DNA
363 <400> SEQUENCE: 7
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369 <211> LENGTH: 41
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377 <220> FEATURE:
379 <223> OTHER INFORMATION: Synthetic DNA
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387 <211> LENGTH: 41
389 <212> TYPE: DNA
391 <213> ORGANISM: Artificial Sequence
395 <220> FEATURE:
397 <223> OTHER INFORMATION: Synthetic DNA
399 <400> SEQUENCE: 9
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405 <211> LENGTH: 41
407 <212> TYPE: DNA
409 <213> ORGANISM: Artificial Sequence
413 <220> FEATURE:
415 <223> OTHER INFORMATION: Synthetic DNA
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423 <211> LENGTH: 41
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427 <213> ORGANISM: Artificial Sequence
431 <220> FEATURE:
433 <223> OTHER INFORMATION: Synthetic DNA
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439 <210> SEQ ID NO: 12
441 <211> LENGTH: 41
443 <212> TYPE: DNA
445 <213> ORGANISM: Artificial Sequence
449 <220> FEATURE:
451 <223> OTHER INFORMATION: Synthetic DNA
453 <400> SEQUENCE: 12
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459 <211> LENGTH: 42
461 <212> TYPE: DNA
463 <213> ORGANISM: Artificial Sequence
467 <220> FEATURE:
469 <223> OTHER INFORMATION: Synthetic DNA
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477 <211> LENGTH: 40
479 <212> TYPE: DNA
481 <213> ORGANISM: Artificial Sequence

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/892,864A

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